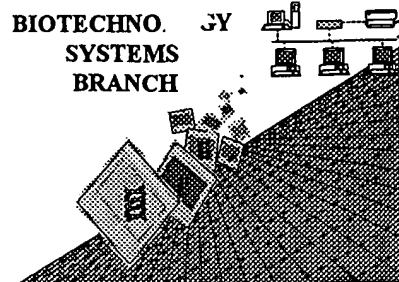


## **RAW SEQUENCE LISTING** **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/593,793  
Source: OIPK  
Date Processed by STIC: 6/20/2000

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**  
**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/593,793

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2      Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3   J   Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4      Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5      Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6      Variable Length      Sequence(s)      contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7      PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)                     . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence.
- 8      Skipped Sequences      Sequence(s)      missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
                    (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
                    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
                    This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9      Skipped Sequences      Sequence(s)      missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
                    <400> sequence id number  
                    000
- 10   J   Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11      Use of <213>Organism      Sequence(s)              are missing this mandatory field or its response.  
(NEW RULES)
- 12      Use of <220>Feature      Sequence(s)      are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13      PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIFE

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/593,793

DATE: 06/20/2000  
 TIME: 12:41:31

Input Set : A:\42715c15:app  
 Output Set: N:\CRF3\06202000\I593793.raw

3 <110> APPLICANT: Xu, Jiangchun  
 4     Dillon, Davin C.  
 5     Mitcham, Jennifer L.  
 6     Harlocker, Susan L.  
 7     Jiang, Yuqui  
 8     Reed, Steven G.  
 9     Kalos, Michael D.  
 10    Fanger, Gary R.  
 11    Retter, Marc W.  
 12    Stolk, John A.  
 13    Day, Craig H.  
 14    Vedvick, Thomas S.  
 15    Carter, Darrick  
 16    Li, Samuel  
 17    Wang, Aijun  
 18    Skeiky, Yasir A.W.  
 19    Helper, William  
 21 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
 22     DIAGNOSIS OF PROSTATE CANCER  
 24 <130> FILE REFERENCE: 210121.42715C15  
 26 <140> CURRENT APPLICATION NUMBER: US/09/593,793  
 27 <141> CURRENT FILING DATE: 2000-06-13  
 29 <160> NUMBER OF SEQ ID NOS: 814  
 31 <170> SOFTWARE: FastSEQ for Windows Version 3.0

Does Not Comply  
 Corrected Diskette Needed

# ERRORED SEQUENCES

676 <210> SEQ ID NO: 26  
 677 <211> LENGTH: 820  
 678 <212> TYPE: DNA  
 679 <213> ORGANISM: Homo sapien  
 681 <220> FEATURE:  
 682 <221> NAME/KEY: misc\_feature  
 683 <222> LOCATION: (1)...(820)  
 684 <223> OTHER INFORMATION: n = A,T,C or G  
 686 <400> SEQUENCE: 26

W--> 687 anattantac agtghtaatct ttccccagag gtgtgtanag ggaacggggc ctagaggcat 60  
 W--> 688 cccanagata ncttatanca acagtgtctt gaccaagagc tgctggggc atttcttgca 120  
 689 gaaaagggtg cggtcccat cactctcct ctcccatagc catcccagag gggtagtag 180  
 W--> 690 ccatacangc ttgggtggga gggagtcang gaaacaacan accacagagc anacagacca 240  
 W--> 691 ntgatgacca tgggcgggag cgagcctctt ccctgnaccg ggggtggcna nganagccta 300  
 W--> 692 nctgaggggt cacactataa acgttaacga ccnagatnan cactgtcttc aagtgcaccc 360  
 W--> 693 ttcctacctg acnaccagng accnnnaact gcngcctggg gacagcctg ggancagcta 420  
 W--> 694 acnnagcact cactgtcccc cccatggcgg tncgctccc tggctcctgnc aagggaagct 480  
 W--> 695 ccctgttgga attncgggga naccaaggga nccccctcct ccactgtga agggaaaann 540  
 W--> 696 gatggaattt tncctctccg gccnntcccc tcttcttta cagccccct nntactentc 600

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/593,793

DATE: 06/20/2000  
 TIME: 12:41:31

Input Set : A:\42715c15.app  
 Output Set : N:\CRF3\06202000\I593793.raw

W--> 697 tccctctntt ntccctgncnc accttttnacc ccnnnatttc ccttnattga tcggannctn 660  
 W--> 698 ganattccac tnnccctnc cntcnatcng naanacnaaa nactntctna ccnggggat 720  
 E--> 699  
 gggnnccctcg ntcatectct ctttttncct accnccnmtt ctttgccctct ccttngatca 780tccaaccntc gntggccntn cccccccnnn tcc

7203 <210> SEQ ID NO: 378  
 7204 <211> LENGTH: 1719  
 7205 <212> TYPE: PRT  
 7206 <213> ORGANISM: Homo sapien  
 7208 <400> SEQUENCE: 378

*pp 4-b* *Insert a hard return*

7209 Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys  
 7210 1 5 10 15  
 7211 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe  
 7212 20 25 30  
 7213 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp  
 7214 35 40 45  
 7215 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp  
 7216 50 55 60  
 7217 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val  
 7218 65 70 75 80  
 7219 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn  
 7220 85 90 95  
 7221 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser  
 7222 100 105 110  
 7223 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe  
 7224 115 120 125  
 7225 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His  
 7226 130 135 140  
 7227 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met  
 7228 145 150 155 160  
 7229 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala  
 7230 165 170 175  
 7231 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu  
 7232 180 185 190  
 7233 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr  
 7234 195 200 205  
 7235 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met  
 7236 210 215 220  
 7237 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn  
 7238 225 230 235 240  
 7239 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys  
 7240 245 250 255  
 7241 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly  
 7242 260 265 270  
 7243 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val  
 7244 275 280 285  
 7245 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr  
 7246 290 295 300  
 7247 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile  
 7248 305 310 315 320  
 7249 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/593,793

DATE: 06/20/2000  
 TIME: 12:41:32

Input Set : A:\42715c15.app  
 Output Set: N:\CRF3\06202000\I593793.raw

```

7250          325          330          335
7251 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
7252          340          345          350
7253 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
7254          355          360          365
7255 Ser Ser Glu Asn Ser Asn Pro Glu Asn Val Ser Arg Thr Arg Asn Lys
7256          370          375          380
7257 Pro Arg Thr His Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser
7258          385          390          395
7259 Ser Val Lys Lys Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys
7260          405          410          415
7261 Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly
7262          420          425          430
7263 Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys
7264          435          440          445
7265 Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly
7266          450          455          460
7267 Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys
7268          465          470          475
7269 Thr Leu Arg Asn Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys
7270          485          490          495
7271 Cys Arg Gly Ser Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp
7272          500          505          510
7273 Asp Ser Ala Phe Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu
7274          515          520          525
7275 Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp
7276          530          535          540
7277 Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln
7278          545          550          555
7279 Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val
7280          565          570          575
7281 Val Lys Leu Leu Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn
7282          580          585          590
7283 Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu
7284          595          600          605
7285 Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp
7286          610          615          620
7287 Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys
7288          625          630          635
7289 Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys
7290          645          650          655
7291 Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys
7292          660          665          670
7293 Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala
7294          675          680          685
7295 Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly
7296          690          695          700
7297 Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser
7298          705          710          715          720

```

RAW SEQUENCE LISTING                      DATE: 06/20/2000  
 PATENT APPLICATION: US/09/593,793                      TIME: 12:41:32

Input Set : A:\42715c15.app  
 Output Set: N:\CRF3\06202000\I593793.raw

7299 Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser  
 7300                      725                      730                      735  
 7301- His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln  
 7302                      740                      745                      750  
 7303 Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys  
 7304                      755                      760                      765  
 7305 Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser  
 7306                      770                      775                      780  
 7307 Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp  
 7308                      785                      790                      795                      800  
 7309 Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly  
 7310                      805                      810                      815  
 7311 Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn  
 7312                      820                      825                      830  
 7313 Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe  
 7314                      835                      840                      845  
 7315 Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser  
 7316                      850                      855                      860  
 7317 Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn  
 7318                      865                      870                      875                      880  
 7319 Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu  
 7320                      885                      890                      895  
 7321 Glu Gly Ser Glu Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile  
 7322                      900                      905                      910  
 7323 Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn  
 7324                      915                      920                      925  
 7325 Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro  
 7326                      930                      935                      940  
 7327 Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu  
 7328                      945                      950                      955                      960  
 7329 Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe  
 7330                      965                      970                      975  
 7331 Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His  
 7332                      980                      985                      990  
 7333 Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser  
 7334                      995                      1000                      1005  
 7335 Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu  
 7336                      1010                      1015                      1020  
 7337 Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His  
 E--> 7338 1025                      1030                      1035                      1040  
 7339 Gln Ser Gln Leu Pro Arg Thr His Met Val Val Glu Val Asp Ser Met  
 7340                      1045                      1050                      1055  
 7341 Pro Ala Ala Ser Ser Val Lys Lys Pro Phe Gly Leu Arg Ser Lys Met  
 7342                      1060                      1065                      1070  
 7343 Gly Lys Trp Cys Cys Arg Cys Phe Pro Cys Cys Arg Glu Ser Gly Lys  
 7344                      1075                      1080                      1085  
 7345 Ser Asn Val Gly Thr Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr  
 7346                      1090                      1095                      1100  
 7347 Leu Arg Ser Lys Met Gly Lys Trp Cys Arg His Cys Phe Pro Cys Cys

when amino acid  
 number is under  
 the last amino  
 acid, end number  
 under the last  
 letter of the  
 amino acid.  
 (e.g. His  
 1040)

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/593,793

DATE: 06/20/2000  
 TIME: 12:41:32

Input Set : A:\42715c15.app  
 Output Set: N:\CRF3\06202000\I593793.raw

```

E--> 7348 1105          1110          1115          112
7349 Arg Gly Ser Gly Lys Ser Asn Val Gly Ala Ser Gly Asp His Asp Asp
7350          1125          1130          1135
7351 Ser Ala Met Lys Thr Leu Arg Asn Lys Met Gly Lys Trp Cys Cys His
7352          1140          1145          1150
7353 Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Lys Val Gly Ala Trp
7354          1155          1160          1165
7355 Gly Asp Tyr Asp Asp Ser Ala Phe Met Glu Pro Arg Tyr His Val Arg
7356          1170          1175          1180
7357 Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val
E--> 7358 1185          1190          1195          120
7359 Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys
7360          1205          1210          1215
7361 Lys Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly
7362          1220          1225          1230
7363 Asn Ser Glu Val Val Lys Leu Leu Asp Arg Arg Cys Gln Leu Asn
7364          1235          1240          1245
7365 Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Ile Lys Ala Val Gln Cys
7366          1250          1255          1260
7367 Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro
E--> 7368 1265          1270          1275          128
7369 Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Ile Tyr
7370          1285          1290          1295
7371 Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp
7372          1300          1305          1310
7373 Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Leu Gly Val
7374          1315          1320          1325
7375 His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala
7376          1330          1335          1340
7377 Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala
E--> 7378 1345          1350          1355          136
7379 Val Cys Cys Gly Ser Ala Ser Ile Val Ser Leu Leu Leu Glu Gln Asn
7380          1365          1370          1375
7381 Ile Asp Val Ser Ser Gln Asp Leu Ser Gly Gln Thr Ala Arg Glu Tyr
7382          1380          1385          1390
7383 Ala Val Ser Ser His His His Val Ile Cys Gln Leu Leu Ser Asp Tyr
7384          1395          1400          1405
7385 Lys Glu Lys Gln Met Leu Lys Ile Ser Ser Glu Asn Ser Asn Pro Glu
7386          1410          1415          1420
7387 Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Phe Lys Gly
E--> 7388 1425          1430          1435          144
7389 Ser Glu Asn Ser Gln Pro Glu Lys Met Ser Gln Glu Pro Glu Ile Asn
7390          1445          1450          1455
7391 Lys Asp Gly Asp Arg Glu Val Glu Glu Glu Met Lys Lys His Glu Ser
7392          1460          1465          1470
7393 Asn Asn Val Gly Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly
7394          1475          1480          1485
7395 Asn Gly Asp Asn Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu
7396          1490          1495          1500

```

*Same  
 Enon*

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/593,793

DATE: 06/20/2000  
 TIME: 12:41:32

Input Set : A:\42715c15.app  
 Output Set: N:\CRF3\06202000\I593793.raw

7397 Asn Gln Gln Phe Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys  
 E--> 7398 1505 1510 1515 152  
 7399 Glu Leu Val-Ser Asp Tyr Lys Glu Lys Gln Met. Pro Lys Tyr Ser Ser  
 7400 1525 1530 1535  
 7401 Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu  
 7402 1540 1545 1550  
 7403 Ser Gln Arg Leu Glu Gly Ser Glu Asn Gly Gln Pro Glu Lys Arg Ser  
 7404 1555 1560 1565  
 7405 Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Leu Glu Asn Phe  
 7406 1570 1575 1580  
 7407 Met Ala Ile Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe  
 E--> 7408 1585 1590 1595 160  
 7409 Pro Glu Asn Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly  
 7410 1605 1610 1615  
 7411 Leu Ile Pro Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro  
 7412 1620 1625 1630  
 7413 Asp Thr Glu Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln  
 7414 1635 1640 1645  
 7415 Lys Gln Phe Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile  
 7416 1650 1655 1660  
 7417 Leu Ile His Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser  
 E--> 7418 1665 1670 1675 168  
 7419 Glu Leu Ser Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn  
 7420 1685 1690 1695  
 7421 Ser Thr Leu Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr  
 7422 1700 1705 1710  
 7423 Met Lys His Gln Ser Gln Leu  
 7424 1715  
 7680 <210> SEQ ID NO: 383  
 7681 <211> LENGTH: 155  
 7682 <212> TYPE: PRT  
 7683 <213> ORGANISM: Homo sapiens  
 7685 <400> SEQUENCE: 383  
 7686 Met Ala Gly Val Arg Asp Gln Gly Gln Gly Ala Arg Trp Pro His Thr  
 7687 5 10 15  
 7689 Gly Lys Arg Gly Pro Leu Leu Gln Gly Leu Thr Trp Ala Thr Gly Gly  
 7690 20 25 30  
 7692 His Cys Phe Ser Ser Glu Glu Ser Gly Ala Val Asp Gly Ala Gly Gln  
 7693 35 40 45  
 7695 Lys Lys Asp Arg Ala Trp Leu Arg Cys Pro Glu Ala Val Ala Gly Phe  
 7696 50 55 60  
 7698 Pro Leu Gly Ser Asp Cys Arg Glu Gly Gly Arg Gln Gly Cys Gly Gly  
 7699 65 70 75 80  
 7701 Ser Asp Asp Glu Asp Asp Leu Gly Val Ala Pro Gly Leu Ala Pro Ala  
 7702 85 90 95  
 7704 Trp Ala Leu Thr Gln Pro Pro Ser Gln Ser Pro Gly Pro Gln Ser Leu  
 7705 100 105 110  
 7707 Pro Ser Thr Pro Ser Ser Ile Trp Pro Gln Trp Val Ile Leu Ile Thr  
 7708 115 120 125

*same*

*154 (next page)*



RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/593,793

DATE: 06/20/2000  
 TIME: 12:41:32

Input Set : A:\42715c15.app  
 Output Set: N:\CRF3\06202000\I593793.raw

```

7710 Glu Leu Thr Ile Pro Ser Pro Ala His Gly Pro Pro Trp Leu Pro Asn
7711      130      135      140
7713 Ala Leu Glu Arg Gly His Leu-Val Arg-Glu
E--> 7714 145      150
9515 <210> SEQ ID NO: 477
9516 <211> LENGTH: 141 140
9517 <212> TYPE: PRT
9518 <213> ORGANISM: Homo sapiens
9520 <400> SEQUENCE: 477
9521 Met Asp Gly His Thr Asp Ile Trp Arg Asn His Met Asp Thr Pro Pro
9522      5      10      15
9524 His Tyr His Arg Asp Thr Asp Thr Arg His His His Met Asp Thr
9525      20      25      30
9527 Leu Ser His Tyr His Arg Asp Thr Arg His His Thr Val Thr Trp Thr
9528      35      40      45
9530 His His His Thr His Glu His Thr Asp Thr Leu Pro Tyr Gly His Trp
9531      50      55      60
9533 His Thr His Cys His Thr Val Thr Trp Thr His Leu His Thr Ile Thr
9534      65      70      75      80
9536 Pro Pro His Thr Leu Pro Val Asp Thr Arg Thr His Arg His Cys His
9537      85      90      95
9539 Thr Asp Thr Gln Asn Thr Val Thr Arg Arg His His His Ala Asp Thr
9540      100      105      110
9542 Pro Pro Leu Trp Cys Arg Leu Asn Tyr Pro Ala Gly Gly Thr Ala Val
9543      115      120      125
9545 Ala Tyr Ser Cys Leu Ser Asp Trp Leu Ser Pro Gln
E--> 9546      130      135      140
9549 <210> SEQ ID NO: 478
9550 <211> LENGTH: 144 143
9551 <212> TYPE: PRT
9552 <213> ORGANISM: Homo sapiens
9554 <400> SEQUENCE: 478
9555 Met Tyr Arg His Thr Glu Thr Leu Pro His Gly Asp Thr Val Thr Gln
9556      5      10      15
9558 Ser His Gly His Thr Gly Ile Val Thr Trp Thr Asp Thr Gln Thr Tyr
9559      20      25      30
9561 Gly Glu Ile Thr Trp Thr His His His Thr Ile Thr Gly Thr Gln Thr
9562      35      40      45
9564 His Gly Asp Ile Thr Thr Trp Thr His Cys His Thr Thr Thr Gly Thr
9565      50      55      60
9567 Arg Asp Ile Thr Leu Ser His Gly His Thr Ile Thr His Met Asn Thr
9568      65      70      75      80
9570 Pro Thr His Cys His Met Asp Thr Gly Thr His Thr Ala Thr Leu Ser
9571      85      90      95
9573 His Gly His Thr Ser Thr Pro Ser His His His Thr His Cys Leu Trp
9574      100      105      110
9576 Thr Gln Gly His Thr Asp Thr Val Thr Gln Ile His Lys Thr Leu Ser
9577      115      120      125
9579 His Gly Asp Ile Thr Met Gln Ile His His His Ser Gly Ala Val

```

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Input Set : A:\42715c15.app  
 Output Set: N:\CRF3\06202000\I593793.raw

```

E--> 9580      130      135      140
9583 <210> SEQ ID NO: 479
9584 <211> LENGTH: 223
9585 <212> TYPE: PRT
9586 <213> ORGANISM: Homo sapiens
9588 <400> SEQUENCE: 479
9589 Met Tyr Arg His Thr Glu Thr Leu Pro His Gly Asp Thr Val Thr Gln
9590                      5                      10                      15
9592 Ser His Glu His Thr Gly Ile Val Thr Trp Thr Asp Thr Gln Thr Tyr
9593                      20                      25                      30
9595 Gly Glu Ile Thr Leu Thr His His His Thr Ile Thr Gly Thr Gln Thr
9596                      35                      40                      45
9598 His Gly Asp Ile Thr Thr Trp Thr His Cys His Thr Thr Thr Gly Thr
9599                      50                      55                      60
9601 Arg Asp Ile Thr Leu Ser His Gly His Thr Ile Thr His Met Asn Thr
9602                      65                      70                      75                      80
9604 Pro Thr His Cys His Met Asp Thr Ala Thr His Thr Ala Thr Leu Ser
9605                      85                      90                      95
9607 His Gly His Thr Ser Ile Pro Ser His His His Thr His Cys His Val
9608                      100                     105                     110
9610 Asp Thr Arg Thr His Arg His Cys His Thr Asp Thr Gln Asn Thr Val
9611                      115                     120                     125
9613 Thr Arg Arg His His His Ala Asp Thr Pro Pro His Gly His Ser Thr
9614                      130                     135                     140
9616 Arg His Ser Ala Thr Gln Ile His His His Thr Glu Met Arg Thr His
9617                      145                     150                     155                     160
9619 Cys His Thr Asp Thr Thr Thr Ser Leu Pro His Phe His Val Ser Ala
9620                      165                     170                     175
9622 Gly Gly Val Gly Pro Thr Thr Leu Gly Ser Asn Arg Glu Ile Thr Trp
9623                      180                     185                     190
9625 Thr Tyr Ser Glu Gly Lys Ile Phe Phe Tyr Phe Leu Gly Asn Gln Ala
9626                      195                     200                     205
9628 Arg Leu Cys Leu Lys Lys Arg Lys Lys Lys Gln Tyr Thr Val
E--> 9629      210      215      220
9632 <210> SEQ ID NO: 480
9633 <211> LENGTH: 145
9634 <212> TYPE: PRT
9635 <213> ORGANISM: Homo sapiens
9637 <400> SEQUENCE: 480
9638 Met Glu Pro Tyr Arg Gly Asn Glu Gln Pro Ser Gln Glu Gln Gly Val
9639                      5                      10                      15
9641 Cys Cys Leu Trp Gly Leu Gln Ser Leu Pro Gln Gly Ser Tyr Val Thr
9642                      20                      25                      30
9644 Val Gly Phe Leu Val Val Lys Arg Gln Thr Ile Gly Arg Leu Glu Arg
9645                      35                      40                      45
9647 Asp Phe Met Phe Lys Cys Arg Lys Gln Pro Gly Leu Pro Pro Ser Gly
9648                      50                      55                      60
9650 Leu Cys Leu Leu Trp Pro Trp Pro Asn Leu Glu Phe Gly Arg Arg Gln
9651                      65                      70                      75                      80

```

RAW SEQUENCE LISTING  
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 TIME: 12:41:32

Input Set : A:\42715c15.app  
 Output Set: N:\CRF3\06202000\I593793.raw

```

9653 Asp Arg Leu Thr Trp Ser Ser Val Ser Val Ala Gly Val Cys Ala Cys
9654                      85                      90                      95
9656 Arg Ala Arg Pro Gly Trp Leu-Gly Glu Gln Pro Ala Thr Ser Ala Gly
9657                      100                      105                      110
9659 Val Arg Leu Glu Gln Val Glu Gln Pro Pro Ala His Pro Leu Gln Glu
9660                      115                      120                      125
9662 Ala Gly Val Ala Arg Phe Pro Arg Pro Glu Trp Val Pro Pro Asn Gly
E--> 9663          130                      135                      140
9669 <210> SEQ ID NO: 481
9670 <211> LENGTH: 168
9671 <212> TYPE: PRT
9672 <213> ORGANISM: Homo sapiens
9674 <400> SEQUENCE: 481
9675 Met His Gly Pro Gln Val Leu Ala Arg Cys Ser Glu Cys Ala Cys Pro
9676                      5                      10                      15
9678 Ala Leu Ala Ala Thr Ser Ala Gly Val Arg Leu Glu Gly Val Asp Arg
9679                      20                      25                      30
9681 Pro Pro Thr Leu Pro Ser Gln Gly Ser Gly Trp Pro Cys Ser His Ser
9682                      35                      40                      45
9684 Leu Ser Gly Cys His Leu Met Ala Asp Gly Ala Lys Ala Leu Gly Lys
9685                      50                      55                      60
9687 Ala Asp Gly Pro Trp Pro Tyr Leu Phe Val Arg Arg Thr Asp Val Pro
9688                      65                      70                      75                      80
9690 Cys Pro Ala Ala Ser Glu Val Gly Gly Cys Ala Pro Ser Ser Trp Arg
9691                      85                      90                      95
9693 Ala Leu Ala Glu Val Thr Gly Cys Ser Leu Gly Pro Leu Gly Leu Ala
9694                      100                     105                     110
9696 Gln His Ala Gln Ala Ser Val Leu Leu Cys Tyr Lys Trp Ser His
9697                      115                     120                     125
9699 Ile Gly Glu Thr Ser Ser His Leu Arg Ser Lys Val Tyr Ala Ala Phe
9700                      130                     135                     140
9702 Gly Gly Ser Ser Pro Cys Leu Lys Gly Leu Met Ser Leu Trp Ala Ser
9703 145                      150                      155                      160
9705 Trp Leu Ser Arg Gly Arg Pro
E--> 9706          165
9709 <210> SEQ ID NO: 482
9710 <211> LENGTH: 144
9711 <212> TYPE: PRT
9712 <213> ORGANISM: Homo sapiens
9714 <400> SEQUENCE: 482
9715 Met Glu Pro Tyr Arg Gly Asn Lys Lys Gln Val Gln Glu Lys Gly Val
9716                      5                      10                      15
9718 Pro Cys Leu Trp Gly Ser Ser Pro Cys Leu Arg Cys His Met Ala Leu
9719                      20                      25                      30
9721 Arg Ala Ser Trp Leu Pro Gly Gly Gly Pro Gln Ala Ile Leu Gly Arg
9722                      35                      40                      45
9724 Thr Leu Cys Ser Ser Ala Glu Ser Ser Gln Asp Cys His Pro Gly Gly
9725                      50                      55                      60
9727 Pro Ser Ile Ala Leu Ala Lys Pro Cys Arg Gly Val Trp Leu Leu Phe

```

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Input Set : A:\42715c15.app  
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```

9728 65                               70                               75                               80
9730 Glu Pro Ala Trp Pro Pro Trp His Ala Arg Ala Pro Gly Ala Gly Thr
9731 - - - 85 - - - 90 - - - 95
9733 Leu Leu Arg Val Cys Leu Ser Cys Leu Gly Cys His Leu Cys Gly Gly
9734 100 105 110
9736 Ala Ser Gly Gly Gly Pro Ala Thr Asn Leu Thr Gln Ser Arg Lys
9737 115 120 125
9739 Trp Met Ala Met Phe Pro Gln Pro Glu Trp Leu Pro Pro Asp Gly
E--> 9740 130 135 140
9743 <210> SEQ ID NO: 483
9744 <211> LENGTH: 144 143
9745 <212> TYPE: PRT
9746 <213> ORGANISM: Homo sapiens
9748 <400> SEQUENCE: 483
9749 Met Glu Thr Gln Arg Gly Asn Lys Gln Arg Ala Gln Glu Gln Gly Val
9750 5 10 15
9752 Cys Cys Leu Trp Gly Ser Ser Pro Cys Leu Gly Ser Tyr Gly Thr Ala
9753 20 25 30
9755 Gly Phe Leu Val Ala Lys Arg Arg Thr Thr Gly Leu Leu Glu Glu Asp
9756 35 40 45
9758 Phe Thr Phe Lys Cys Arg Lys Gln Pro Lys Leu Pro Ser Met Arg Leu
9759 50 55 60
9761 Ser Leu Leu Trp Pro Trp Arg Asp Leu Lys Phe Val Pro Arg Gln Asp
9762 65 70 75 80
9764 Lys Leu Thr Arg Ser Ser Val Ser Val Ala Gly Ala Tyr Ala Cys Arg
9765 85 90 95
9767 Ala Gly Pro Gly Trp Leu Lys Glu Gln Pro Ala Thr Ser Ala Arg Val
9768 100 105 110
9770 Arg Leu Val Gln Ala Glu His Pro Pro Pro His Pro Leu Glu Glu Val
9771 115 120 125
9773 Gly Met Ala Arg Phe Pro Gln Pro Glu Cys Leu Pro Pro Tyr Cys
E--> 9774 130 135 140
10291 <210> SEQ ID NO: 523
10292 <211> LENGTH: 254
10293 <212> TYPE: PRT
10294 <213> ORGANISM: Artificial Sequence
10296 <220> FEATURE:
10297 <223> OTHER INFORMATION: Made in a lab
10299 <400> SEQUENCE: 523
10300 Met Ala Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile
10301 1 5 10 15
10302 Leu Gly Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile
10303 20 25 30
10304 Asn Gly Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu
10305 35 40 45
10306 Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln
10307 50 55 60
10308 Trp Val Leu Ser Ala Thr His Cys Phe Gln Asn Ser Tyr Thr Ile Gly
10309 65 70 75 80

```

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Input Set : A:\42715c15.app

Output Set: N:\CRF3\06202000\I593793.raw

10310 Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met  
 10311 85 90 95  
 10312 Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu  
 10313 100 105 110  
 10314 Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu  
 10315 115 120 125  
 10316 Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala  
 10317 130 135 140  
 10318 Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg  
 10319 145 150 155 160  
 10320 Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu  
 10321 165 170 175  
 10322 Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys  
 10323 180 185  
 W--> 10324 Ala Gly Gly Gly Gln Xaa Gln Xaa Asp Ser Cys Asn Gly Asp Ser Gly  
 10325 195 200 205  
 10326 Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly  
 10327 210 215 220  
 10328 Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu  
 10329 225 230 235 240  
 10330 Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser  
 E--> 10331 245 250 250  
 10353 <210> SEQ ID NO: 525  
 10354 <211> LENGTH: 254  
 10355 <212> TYPE: PRT  
 10356 <213> ORGANISM: Homo sapien  
 10358 <400> SEQUENCE: 525  
 10359 Met Ala Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile  
 10360 1 5 10 15  
 10361 Leu Gly Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile  
 10362 20 25 30  
 10363 Asn Gly Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu  
 10364 35 40 45  
 10365 Val Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln  
 10366 50 55 60  
 10367 Trp Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly  
 10368 65 70 75 80  
 10369 Leu Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met  
 10370 85 90 95  
 10371 Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu  
 10372 100 105 110  
 10373 Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu  
 10374 115 120 125  
 10375 Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala  
 10376 130 135 140  
 10377 Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg  
 10378 145 150 155 160  
 10379 Met Pro Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu  
 10380 165 170 175

see item 10 on  
 Ena summary  
 sheet  
 misaligned nos. -  
 see item 4  
 on Ena summary sheet

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Input Set : A:\42715c15.app  
 Output Set: N:\CRF3\06202000\I593793.raw

10381 Val Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys  
 10382                      180                      185                      190  
 10383 Ala Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly  
 10384                      195                      200                      205  
 10385 Gly Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly  
 10386                      210                      215                      220  
 10387 Lys Ala Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu  
 10388 225                      230                      235                      240  
 10389 Cys Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser  
 E--> 10390 245 250 *same even*  
 10416 <210> SEQ ID NO: 527  
 10417 <211> LENGTH: 321 *320*  
 10418 <212> TYPE: PRT  
 10419 <213> ORGANISM: Homo sapiens  
 10421 <400> SEQUENCE: 527  
 10422 Met Ser Ser Cys Asn Phe Thr His Ala Thr Phe Val Leu Ile Gly Ile  
 10423                      5                      10                      15  
 10425 Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser  
 10426                      20                      25                      30  
 10428 Met Tyr Val Val Ala Met Phe Gly Asn Cys Ile Val Val Phe Ile Val  
 10429                      35                      40                      45  
 10431 Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met  
 10432                      50                      55                      60  
 10434 Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile  
 10435                      65                      70                      75                      80  
 10437 Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Phe Glu Ala Cys  
 10438                      85                      90                      95  
 10440 Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr  
 10441                      100                      105                      110  
 10443 Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro  
 10444                      115                      120                      125  
 10446 Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly  
 10447                      130                      135                      140  
 10449 Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Pro Leu Pro Leu  
 10450 145                      150                      155                      160  
 10452 Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser  
 10453                      165                      170                      175  
 10455 Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Ala Asp Thr Leu  
 10456                      180                      185                      190  
 10458 Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val  
 10459                      195                      200                      205  
 10461 Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Thr Val  
 10462                      210                      215                      220  
 10464 Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys  
 10465 225                      230                      235                      240  
 10467 Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly  
 10468                      245                      250                      255  
 10470 Leu Ser Val Val His Arg Phe Gly Asn Ser Leu His Pro Ile Val Arg  
 10471                      260                      265                      270

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```

10473 Val Val Met Gly Asp Ile Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
10474          275          280          285
10476 Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
10477          290          295          300
10479 Met Phe Lys Ile Ser Cys Asp Lys Asp Leu Gln Ala Val Gly Gly Lys
E--> 10480 305          310          315          320
10558 <210> SEQ ID NO: 532
10559 <211> LENGTH: 293 292
10560 <212> TYPE: PRT
10561 <213> ORGANISM: Homo sapiens
10563 <400> SEQUENCE: 532
10564 Met His Leu Ser Phe Pro Ala Phe Leu Pro Pro Trp Met Asp Arg Gly
10565          5          10          15
10567 Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp His Asn Asp Ser Ser
10568          20          25          30
10570 Val Lys Thr Leu Gly Ser Lys Arg Cys Lys Trp Cys Cys His Cys Phe
10571          35          40          45
10573 Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val Val Ala Trp Gly Asp
10574          50          55          60
10576 Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr His Val His Gly Glu
10577          65          70          75          80
10579 Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp Gly Lys Val Pro Arg
10580          85          90          95
10582 Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Arg Asp
10583          100          105          110
10585 Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser
10586          115          120          125
10588 Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys Gln Leu Asn Val Leu
10589          130          135          140
10591 Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala Val Gln Cys Gln Glu
10592 145          150          155          160
10594 Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile
10595          165          170          175
10597 Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Val Tyr Asn Glu
10598          180          185          190
10600 Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu
10601          195          200          205
10603 Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu Gly Ile His Glu
10604          210          215          220
10606 Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu
10607 225          230          235          240
10609 Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu Ile Leu Ala Val Cys
10610          245          250          255
10612 Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu Glu Gln Asn Val Asp
10613          260          265          270
10615 Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu Ser Met Leu Phe Leu
10616          275          280          285
10618 Val Ile Ile Met
E--> 10619          290

```

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Input Set : A:\42715c15.app  
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10643 <210> SEQ ID NO: 534  
 10644 <211> LENGTH: 267 **266**  
 10645 <212> TYPE: PRT  
 10646 <213> ORGANISM: Homo sapiens  
 10648 <400> SEQUENCE: 534  
 10649 Met Tyr Lys Leu Gln Cys Asn Asn Cys Ala Thr Asn Gly Ala Thr Glu  
 10650 5 10 15  
 10652 Arg Lys Gln Ala Ala Gly Ser Gly Ala Gly Tyr Ala Leu Pro Ser Ala  
 10653 20 25 30  
 10655 Leu Gln Ser Met Pro Gln Gly Ser Tyr Ala Thr Ala Arg Phe Leu Val  
 10656 35 40 45  
 10658 Ala Lys Arg Pro Thr Thr Gly His Leu Glu Lys Glu Phe Met Phe His  
 10659 50 55 60  
 10661 Cys Arg Lys Gln Pro Gly Ser Pro Ser Arg Gly Leu Gly Leu Leu Trp  
 10662 65 70 75 80  
 10664 Pro Trp Pro Asp Ile Glu Phe Val Pro Arg Gln Asp Lys Leu Thr Gln  
 10665 85 90 95  
 10667 Ser Ser Val Leu Val Pro Gln Ile Cys Ala Cys Gln Thr Arg Pro Asn  
 10668 100 105 110  
 10670 Trp Leu Asn Glu Gln Pro Ala Thr Ser Ala Gly Val Arg Leu Glu Glu  
 10671 115 120 125  
 10673 Val Asp Gln Pro Pro Thr Leu Pro Ser Gln Gly Ser Gly Trp Pro Cys  
 10674 130 135 140  
 10676 Ser His Ser Leu Ser Gly Cys His Leu Met Ala Asp Ile Ala Lys Ala  
 10677 145 150 155 160  
 10679 Leu Gly Lys Ala Asp Gly Pro Trp Pro Tyr Leu Phe Val Arg Arg Thr  
 10680 165 170 175  
 10682 Asp Val Pro Cys Pro Ala Ala Ser Glu Val Gly Gly Cys Ala Pro Ser  
 10683 180 185 190  
 10685 Ser Trp His Thr Leu Ala Glu Val Thr Gly Cys Ser Leu Ser Pro Leu  
 10686 195 200 205  
 10688 Ser Leu Ala Gln His Ala Gln Ala Ser Val Leu Leu Leu Cys Tyr Lys  
 10689 210 215 220  
 10691 Trp Ser His Ile Gly Glu Thr Ser Ser His Leu Arg Ser Lys Val Tyr  
 10692 225 230 235 240  
 10694 Ala Ala Phe Gly Gly Ser Ser Pro Cys Leu Lys Gly Leu Met Ser Leu  
 10695 245 250 255  
 10697 Trp Ala Ser Trp Leu Pro Arg Gly Arg Pro  
 E--> 10698 260 265  
 10925 <210> SEQ ID NO: 537  
 10926 <211> LENGTH: 1229 **1228 pp. 17-18**  
 10927 <212> TYPE: PRT  
 10928 <213> ORGANISM: Homo sapiens  
 10930 <400> SEQUENCE: 537  
 10931 Met Leu Pro Val Tyr Gln Glu Val Lys Pro Asn Pro Leu Gln Asp Ala  
 10932 5 10 15  
 10934 Asn Leu Cys Ser Arg Val Phe Phe Trp Trp Leu Asn Pro Leu Phe Lys  
 10935 20 25 30  
 10937 Ile Gly His Lys Arg Arg Leu Glu Glu Asp Asp Met Tyr Ser Val Leu



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Input Set : A:\42715c15.app  
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```

10938      35      40      45
10940 Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu Leu Gln Gly Phe Trp
10941      50      55      60
10943 Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala Gln Lys Pro Ser Leu
10944      65      70      75      80
10946 Thr Arg Ala Ile Ile Lys Cys Tyr Trp Lys Ser Tyr Leu Val Leu Gly
10947      85      90      95
10949 Ile Phe Thr Leu Ile Glu Glu Ser Ala Lys Val Ile Gln Pro Ile Phe
10950      100     105     110
10952 Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr Asp Pro Met Asp Ser
10953      115     120     125
10955 Val Ala Leu Asn Thr Ala Tyr Ala Thr Val Leu Thr Phe Cys
10956      130     135     140
10958 Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr Phe Tyr His Val Gln
10959      145     150     155     160
10961 Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys His Met Ile Tyr Arg
10962      165     170     175
10964 Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly Lys Thr Thr Thr Gly
10965      180     185     190
10967 Gln Ile Val Asn Leu Leu Ser Asn Asp Val Asn Lys Phe Asp Gln Val
10968      195     200     205
10970 Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro Leu Gln Ala Ile Ala
10971      210     215     220
10973 Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile Ser Cys Leu Ala Gly
10974      225     230     235     240
10976 Met Ala Val Leu Ile Ile Leu Leu Pro Leu Gln Ser Cys Phe Gly Lys
10977      245     250     255
10979 Leu Phe Ser Ser Leu Arg Ser Lys Thr Ala Thr Phe Thr Asp Ala Arg
10980      260     265     270
10982 Ile Arg Thr Met Asn Glu Val Ile Thr Gly Ile Arg Ile Ile Lys Met
10983      275     280     285
10985 Tyr Ala Trp Glu Lys Ser Phe Ser Asn Leu Ile Thr Asn Leu Arg Lys
10986      290     295     300
10988 Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys Leu Arg Gly Met Asn
10989      305     310     315     320
10991 Leu Ala Ser Phe Phe Ser Ala Ser Lys Ile Ile Val Phe Val Thr Phe
10992      325     330     335
10994 Thr Thr Tyr Val Leu Leu Gly Ser Val Ile Thr Ala Ser Arg Val Phe
10995      340     345     350
10997 Val Ala Val Thr Leu Tyr Gly Ala Val Arg Leu Thr Val Thr Leu Phe
10998      355     360     365
11000 Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala Ile Val Ser Ile Arg
11001      370     375     380
11003 Arg Ile Gln Thr Phe Leu Leu Asp Glu Ile Ser Gln Arg Asn Arg
11004      385     390     395     400
11006 Gln Leu Pro Ser Asp Gly Lys Lys Met Val His Val Gln Asp Phe Thr
11007      405     410     415
11009 Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr Leu Gln Gly Leu Ser
11010      420     425     430

```

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```

11012 Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val Val Gly Pro Val Gly
11013      435      440      445
11015 Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu Gly Glu Leu Ala Pro
11016      450      455      460
11018 Ser His Gly Leu Val Ser Val His Gly Arg Ile Ala Tyr Val Ser Gln
11019 465      470      475      480
11021 Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser Asn Ile Leu Phe Gly
11022      485      490      495
11024 Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val Ile Lys Ala Cys Ala
11025      500      505      510
11027 Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly Asp Leu Thr Val Ile
11028      515      520      525
11030 Gly Asp Arg Gly Thr Thr Leu Ser Gly Gly Gln Lys Ala Arg Val Asn
11031      530      535      540
11033 Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile Tyr Leu Leu Asp Asp
11034 545      550      555      560
11036 Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg His Leu Phe Glu Leu
11037      565      570      575
11039 Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr Ile Leu Val Thr His
11040      580      585      590
11042 Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile Leu Ile Leu Lys Asp
11043      595      600      605
11045 Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu Phe Leu Lys Ser Gly
11046      610      615      620
11048 Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn Glu Glu Ser Glu Gln
11049 625      630      635      640
11051 Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn Arg Thr Phe Ser Glu
11052      645      650      655
11054 Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro Ser Leu Lys Asp Gly
11055      660      665      670
11057 Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro Val Thr Leu Ser Glu
11058      675      680      685
11060 Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln Ala Tyr Lys Asn Tyr
11061      690      695      700
11063 Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile Phe Leu Ile Leu Leu
11064 705      710      715      720
11066 Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln Asp Trp Trp Leu Ser
11067      725      730      735
11069 Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val Thr Val Asn Gly Gly
11070      740      745      750
11072 Gly Asn Val Thr Glu Lys Leu Asp Leu Asn Trp Tyr Leu Gly Ile Tyr
11073      755      760      765
11075 Ser Gly Leu Thr Val Ala Thr Val Leu Phe Gly Ile Ala Arg Ser Leu
11076      770      775      780
11078 Leu Val Phe Tyr Val Leu Val Asn Ser Ser Gln Thr Leu His Asn Lys
11079 785      790      795      800
11081 Met Phe Glu Ser Ile Leu Lys Ala Pro Val Leu Phe Phe Asp Arg Asn
11082      805      810      815
11084 Pro Ile Gly Arg Ile Leu Asn Arg Phe Ser Lys Asp Ile Gly His Leu

```

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/593,793

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Input Set : A:\42715c15.app  
 Output Set: N:\CRF3\06202000\I593793.raw

```

11085      820      825      830
11087 Asp Asp Leu Leu Pro Leu Thr Phe Leu Asp Phe Ile Gln Thr Leu Leu
11088      835      840      845
11090 Gln Val Val Gly Val Val Ser Val Ala Val Ala Val Ile Pro Trp Ile
11091      850      855      860
11093 Ala Ile Pro Leu Val Pro Leu Gly Ile Ile Phe Ile Phe Leu Arg Arg
11094 865      870      875      880
11096 Tyr Phe Leu Glu Thr Ser Arg Asp Val Lys Arg Leu Glu Ser Thr Thr
11097      885      890      895
11099 Arg Ser Pro Val Phe Ser His Leu Ser Ser Leu Gln Gly Leu Trp
11100      900      905      910
11102 Thr Ile Arg Ala Tyr Lys Ala Glu Glu Arg Cys Gln Glu Leu Phe Asp
11103      915      920      925
11105 Ala His Gln Asp Leu His Ser Glu Ala Trp Phe Leu Phe Leu Thr Thr
11106      930      935      940
11108 Ser Arg Trp Phe Ala Val Arg Leu Asp Ala Ile Cys Ala Met Phe Val
11109 945      950      955      960
11111 Ile Ile Val Ala Phe Gly Ser Leu Ile Leu Ala Lys Thr Leu Asp Ala
11112      965      970      975
11114 Gly Gln Val Gly Leu Ala Leu Ser Tyr Ala Leu Thr Leu Met Gly Met
11115      980      985      990
11117 Phe Gln Trp Cys Val Arg Gln Ser Ala Glu Val Glu Asn Met Met Ile
E--> 11118 995      1000      1005
11120 Ser Val Glu Arg Val Ile Glu Tyr Thr Asp Leu Glu Lys Glu Ala Pro
E--> 11121 1010      1015      1020
11123 Trp Glu Tyr Gln Lys Arg Pro Pro Ala Trp Pro His Glu Gly Val
E--> 11124 1025      1030      1035      1040
11126 Ile Ile Phe Asp Asn Val Asn Phe Met Tyr Ser Pro Gly Gly Pro Leu
E--> 11127      1045      1050      1055
11129 Val Leu Lys His Leu Thr Ala Leu Ile Lys Ser Gln Glu Lys Val Gly
E--> 11130      1060      1065      1070
11132 Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Ser Leu Ile Ser Ala Leu
E--> 11133      1075      1080      1085
11135 Phe Arg Leu Ser Glu Pro Glu Gly Lys Ile Trp Ile Asp Lys Ile Leu
E--> 11136 1090      1095      1100
11138 Thr Thr Glu Ile Gly Leu His Asp Leu Arg Lys Lys Met Ser Ile Ile
E--> 11139 1105      1110      1115      1120
11141 Pro Gln Glu Pro Val Leu Phe Thr Gly Thr Met Arg Lys Asn Leu Asp
E--> 11142      1125      1130      1135
11144 Pro Phe Asn Glu His Thr Asp Glu Glu Leu Trp Asn Ala Leu Gln Glu
E--> 11145      1140      1145      1150
11147 Val Gln Leu Lys Glu Thr Ile Glu Asp Leu Pro Gly Lys Met Asp Thr
E--> 11148      1155      1160      1165
11150 Glu Leu Ala Glu Ser Gly Ser Asn Phe Ser Val Gly Gln Arg Gln Leu
E--> 11151 1170      1175      1180
11153 Val Cys Leu Ala Arg Ala Ile Leu Arg Lys Asn Gln Ile Leu Ile Ile
E--> 11154 1185      1190      1195      1200
11156 Asp Glu Ala Thr Ala Asn Val Asp Pro Arg Thr Asp Glu Leu Ile Gln
E--> 11157      1205      1210      1215

```

*misaligned  
 not*

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/593,793

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 TIME: 12:41:33

Input Set : A:\42715c15.app  
 Output Set: N:\CRF3\06202000\I593793.raw

11159 Lys Lys Ser Gly Arg Asn Leu Pro Thr Ala Pro Cys  
 E--> 11160 1220 1225  
 11162 <210> SEQ ID NO: 538-  
 11163 <211> LENGTH: 1262 / 261  
 11164 <212> TYPE: PRT  
 11165 <213> ORGANISM: Homo sapiens  
 11167 <400> SEQUENCE: 538  
 11168 Met Tyr Ser Val Leu Pro Glu Asp Arg Ser Gln His Leu Gly Glu Glu  
 11169 5 10 15  
 11171 Leu Gln Gly Phe Trp Asp Lys Glu Val Leu Arg Ala Glu Asn Asp Ala  
 11172 20 25 30  
 11174 Gln Lys Pro Ser Leu Thr Arg Ala Ile Ile Lys Cys Tyr Trp Lys Ser  
 11175 35 40 45  
 11177 Tyr Leu Val Leu Gly Ile Phe Thr Leu Ile Glu Glu Ser Ala Lys Val  
 11178 50 55 60  
 11180 Ile Gln Pro Ile Phe Leu Gly Lys Ile Ile Asn Tyr Phe Glu Asn Tyr  
 11181 65 70 75 80  
 11183 Asp Pro Met Asp Ser Val Ala Leu Asn Thr Ala Tyr Ala Tyr Ala Thr  
 11184 85 90 95  
 11186 Val Leu Thr Phe Cys Thr Leu Ile Leu Ala Ile Leu His His Leu Tyr  
 11187 100 105 110  
 11189 Phe Tyr His Val Gln Cys Ala Gly Met Arg Leu Arg Val Ala Met Cys  
 11190 115 120 125  
 11192 His Met Ile Tyr Arg Lys Ala Leu Arg Leu Ser Asn Met Ala Met Gly  
 11193 130 135 140  
 11195 Lys Thr Thr Thr Gly Gln Ile Val Asn Leu Leu Ser Asn Asp Val Asn  
 11196 145 150 155 160  
 11198 Lys Phe Asp Gln Val Thr Val Phe Leu His Phe Leu Trp Ala Gly Pro  
 11199 165 170 175  
 11201 Leu Gln Ala Ile Ala Val Thr Ala Leu Leu Trp Met Glu Ile Gly Ile  
 11202 180 185 190  
 11204 Ser Cys Leu Ala Gly Met Ala Val Leu Ile Ile Leu Leu Pro Leu Gln  
 11205 195 200 205  
 11207 Ser Cys Phe Gly Lys Leu Phe Ser Ser Leu Arg Ser Lys Thr Ala Thr  
 11208 210 215 220  
 11210 Phe Thr Asp Ala Arg Ile Arg Thr Met Asn Glu Val Ile Thr Gly Ile  
 11211 225 230 235 240  
 11213 Arg Ile Ile Lys Met Tyr Ala Trp Glu Lys Ser Phe Ser Asn Leu Ile  
 11214 245 250 255  
 11216 Thr Asn Leu Arg Lys Lys Glu Ile Ser Lys Ile Leu Arg Ser Ser Cys  
 11217 260 265 270  
 11219 Leu Arg Gly Met Asn Leu Ala Ser Phe Phe Ser Ala Ser Lys Ile Ile  
 11220 275 280 285  
 11222 Val Phe Val Thr Phe Thr Thr Tyr Val Leu Leu Gly Ser Val Ile Thr  
 11223 290 295 300  
 11225 Ala Ser Arg Val Phe Val Ala Val Thr Leu Tyr Gly Ala Val Arg Leu  
 11226 305 310 315 320  
 11228 Thr Val Thr Leu Phe Phe Pro Ser Ala Ile Glu Arg Val Ser Glu Ala  
 11229 325 330 335

RAW SEQUENCE LISTING  
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 TIME: 12:41:33

Input Set : A:\42715c15.app  
 Output Set: N:\CRF3\06202000\I593793.raw

```

11231 Ile Val Ser Ile Arg Arg Ile Gln Thr Phe Leu Leu Leu Asp Glu Ile
11232          340          345          350
11234 Ser Gln Arg Asn Arg Gln Leu Pro Ser Asp Gly Lys Lys Met Val His
11235          355          360          365
11237 Val Gln Asp Phe Thr Ala Phe Trp Asp Lys Ala Ser Glu Thr Pro Thr
11238          370          375          380
11240 Leu Gln Gly Leu Ser Phe Thr Val Arg Pro Gly Glu Leu Leu Ala Val
11241 385          390          395          400
11243 Val Gly Pro Val Gly Ala Gly Lys Ser Ser Leu Leu Ser Ala Val Leu
11244          405          410          415
11246 Gly Glu Leu Ala Pro Ser His Gly Leu Val Ser Val His Gly Arg Ile
11247          420          425          430
11249 Ala Tyr Val Ser Gln Gln Pro Trp Val Phe Ser Gly Thr Leu Arg Ser
11250          435          440          445
11252 Asn Ile Leu Phe Gly Lys Lys Tyr Glu Lys Glu Arg Tyr Glu Lys Val
11253          450          455          460
11255 Ile Lys Ala Cys Ala Leu Lys Lys Asp Leu Gln Leu Leu Glu Asp Gly
11256 465          470          475          480
11258 Asp Leu Thr Val Ile Gly Asp Arg Gly Thr Thr Leu Ser Gly Gly Gln
11259          485          490          495
11261 Lys Ala Arg Val Asn Leu Ala Arg Ala Val Tyr Gln Asp Ala Asp Ile
11262          500          505          510
11264 Tyr Leu Leu Asp Asp Pro Leu Ser Ala Val Asp Ala Glu Val Ser Arg
11265          515          520          525
11267 His Leu Phe Glu Leu Cys Ile Cys Gln Ile Leu His Glu Lys Ile Thr
11268          530          535          540
11270 Ile Leu Val Thr His Gln Leu Gln Tyr Leu Lys Ala Ala Ser Gln Ile
11271 545          550          555          560
11273 Leu Ile Leu Lys Asp Gly Lys Met Val Gln Lys Gly Thr Tyr Thr Glu
11274          565          570          575
11276 Phe Leu Lys Ser Gly Ile Asp Phe Gly Ser Leu Leu Lys Lys Asp Asn
11277          580          585          590
11279 Glu Glu Ser Glu Gln Pro Pro Val Pro Gly Thr Pro Thr Leu Arg Asn
11280          595          600          605
11282 Arg Thr Phe Ser Glu Ser Ser Val Trp Ser Gln Gln Ser Ser Arg Pro
11283          610          615          620
11285 Ser Leu Lys Asp Gly Ala Leu Glu Ser Gln Asp Thr Glu Asn Val Pro
11286 625          630          635          640
11288 Val Thr Leu Ser Glu Glu Asn Arg Ser Glu Gly Lys Val Gly Phe Gln
11289          645          650          655
11291 Ala Tyr Lys Asn Tyr Phe Arg Ala Gly Ala His Trp Ile Val Phe Ile
11292          660          665          670
11294 Phe Leu Ile Leu Leu Asn Thr Ala Ala Gln Val Ala Tyr Val Leu Gln
11295          675          680          685
11297 Asp Trp Trp Leu Ser Tyr Trp Ala Asn Lys Gln Ser Met Leu Asn Val
11298          690          695          700
11300 Thr Val Asn Gly Gly Gly Asn Val Thr Glu Lys Leu Asp Leu Asn Trp
11301 705          710          715          720
11303 Tyr Leu Gly Ile Tyr Ser Gly Leu Thr Val Ala Thr Val Leu Phe Gly

```

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Input Set : A:\42715c15.app  
 Output Set: N:\CRF3\06202000\I593793.raw

```

11304          725          730          735
11306 Ile Ala Arg Ser Leu Leu Val Phe Tyr Val Leu Val Asn Ser Ser Gln
11307          740 - - - - 745          750 - - - -
11309 Thr Leu His Asn Lys Met Phe Glu Ser Ile Leu Lys Ala Pro Val Leu
11310          755          760          765
11312 Phe Phe Asp Arg Asn Pro Ile Gly Arg Ile Leu Asn Arg Phe Ser Lys
11313          770          775          780
11315 Asp Ile Gly His Leu Asp Asp Leu Leu Pro Leu Thr Phe Leu Asp Phe
11316 785          790          795          800
11318 Ile Gln Thr Leu Leu Gln Val Val Gly Val Val Ser Val Ala Val Ala
11319          805          810          815
11321 Val Ile Pro Trp Ile Ala Ile Pro Leu Val Pro Leu Gly Ile Ile Phe
11322          820          825          830
11324 Ile Phe Leu Arg Arg Tyr Phe Leu Glu Thr Ser Arg Asp Val Lys Arg
11325          835          840          845
11327 Leu Glu Ser Thr Thr Arg Ser Pro Val Phe Ser His Leu Ser Ser Ser
11328          850          855          860
11330 Leu Gln Gly Leu Trp Thr Ile Arg Ala Tyr Lys Ala Glu Glu Arg Cys
11331 865          870          875          880
11333 Gln Glu Leu Phe Asp Ala His Gln Asp Leu His Ser Glu Ala Trp Phe
11334          885          890          895
11336 Leu Phe Leu Thr Thr Ser Arg Trp Phe Ala Val Arg Leu Asp Ala Ile
11337          900          905          910
11339 Cys Ala Met Phe Val Ile Ile Val Ala Phe Gly Ser Leu Ile Leu Ala
11340          915          920          925
11342 Lys Thr Leu Asp Ala Gly Gln Val Gly Leu Ala Leu Ser Tyr Ala Leu
11343          930          935          940
11345 Thr Leu Met Gly Met Phe Gln Trp Cys Val Arg Gln Ser Ala Glu Val
11346 945          950          955          960
11348 Glu Asn Met Met Ile Ser Val Glu Arg Val Ile Glu Tyr Thr Asp Leu
11349          965          970          975
11351 Glu Lys Glu Ala Pro Trp Glu Tyr Gln Lys Arg Pro Pro Pro Ala Trp
11352          980          985          990
11354 Pro His Glu Gly Val Ile Ile Phe Asp Asn Val Asn Phe Met Tyr Ser
E--> 11355          995          1000          1005
11357 Pro Gly Gly Pro Leu Val Leu Lys His Leu Thr Ala Leu Ile Lys Ser
E--> 11358          1010          1015          1020
11360 Gln Glu Lys Val Gly Ile Val Gly Arg Thr Gly Ala Gly Lys Ser Ser
E--> 11361 1025          1030          1035          1040
11363 Leu Ile Ser Ala Leu Phe Arg Leu Ser Glu Pro Glu Gly Lys Ile Trp
E--> 11364          1045          1050          1055
11366 Ile Asp Lys Ile Leu Thr Thr Glu Ile Gly Leu His Asp Leu Arg Lys
E--> 11367          1060          1065          1070
11369 Lys Met Ser Ile Ile Pro Gln Glu Pro Val Leu Phe Thr Gly Thr Met
E--> 11370          1075          1080          1085
11372 Arg Lys Asn Leu Asp Pro Phe Asn Glu His Thr Asp Glu Glu Leu Trp
E--> 11373          1090          1095          1100
11375 Asn Ala Leu Gln Glu Val Gln Leu Lys Glu Thr Ile Glu Asp Leu Pro
E--> 11376 1105          1110          1115          1120

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 pos.*

RAW SEQUENCE LISTING  
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 DATE: 06/20/2000  
 TIME: 12:41:33

Input Set : A:\42715c15.app  
 Output Set: N:\CRF3\06202000\I593793.raw

11378 Gly Lys Met Asp Thr Glu Leu Ala Glu Ser Gly Ser Asn Phe Ser Val  
 E--> 11379 1125 1130 1135  
 11381 Gly Gln Arg Gln Leu Val Cys Leu Ala Arg Ala Ile Leu Arg Lys Asn  
 E--> 11382 1140 1145 1150  
 11384 Gln Ile Leu Ile Ile Asp Glu Ala Thr Ala Asn Val Asp Pro Arg Thr  
 E--> 11385 1155 1160 1165  
 11387 Asp Glu Leu Ile Gln Lys Lys Ile Arg Glu Lys Phe Ala His Cys Thr  
 E--> 11388 1170 1175 1180  
 11390 Val Leu Thr Ile Ala His Arg Leu Asn Thr Ile Ile Asp Ser Asp Lys  
 E--> 11391 1185 1190 1195 1200  
 11393 Ile Met Val Leu Asp Ser Gly Arg Leu Lys Glu Tyr Asp Glu Pro Tyr  
 E--> 11394 1205 1210 1215  
 11396 Val Leu Leu Gln Asn Lys Glu Ser Leu Phe Tyr Lys Met Val Gln Gln  
 E--> 11397 1220 1225 1230  
 11399 Leu Gly Lys Ala Glu Ala Ala Ala Leu Thr Glu Thr Ala Lys Gln Arg  
 E--> 11400 1235 1240 1245  
 11402 Trp Gly Phe Thr Met Leu Ala Arg Leu Val Ser Asn Ser  
 E--> 11403 1250 1255 1260  
 11553 <210> SEQ ID NO: 551  
 11554 <211> LENGTH: 15  
 11555 <212> TYPE: PRT  
 11556 <213> ORGANISM: Artificial Sequence  
 11558 <220> FEATURE:  
 11559 <223> OTHER INFORMATION: Made in a lab  
 11561 <400> SEQUENCE: 551  
 E--> 11562 Phe Asp Lys Ser Asp Leu Ala Lys Tyr Ser Ala  
 12135 <210> SEQ ID NO: 574  
 12136 <211> LENGTH: 63  
 12137 <212> TYPE: PRT  
 12138 <213> ORGANISM: Homo sapiens  
 12140 <400> SEQUENCE: 574  
 12141 Met Thr His Ser Ser Ala Trp Leu Glu Arg Pro Gln Glu Thr Tyr Asn  
 12142 5 10 15  
 12144 His Gly Gly Arg Arg Arg Gly Ser Lys Ala Arg Leu Thr Trp Trp Gln  
 12145 20 25 30  
 12147 Glu Arg Thr Ser Glu Gly Gly Asp Cys His Lys Leu Phe Phe Phe Glu  
 12148 35 40 45  
 12150 Thr Arg Val Trp Pro Cys Cys Pro Gly Trp Ser Ala Val Ala  
 E--> 12151 50 55 60  
 12154 <210> SEQ ID NO: 575  
 12155 <211> LENGTH: 77  
 12156 <212> TYPE: PRT  
 12157 <213> ORGANISM: Homo sapiens  
 12159 <400> SEQUENCE: 575  
 12160 Met Val Lys Ser Arg Phe Thr Lys Asn Thr Lys Ile Thr Gln Ala Trp  
 12161 5 10 15  
 12163 Trp Arg Ala Pro Val Ile Pro Gly Thr Arg Glu Ala Glu Gly Gly Glu  
 12164 20 25 30  
 12166 Ser Leu Glu Pro Gly Arg Leu Arg Glu Glu Asn Arg Leu Asn Pro Gly

*None  
even*

*number the amino acids  
under every 5  
amino acids*

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Input Set : A:\42715c15.app  
 Output Set: N:\CRF3\06202000\I593793.raw

```

12167      35      40      45
12169 Gly Arg Gly Cys Ser Glu Pro Arg Ser Cys Cys Cys Thr Pro Ala Trp
12170      50      -55      -60
12172 Ser Thr Glu Gln Asp Ser Ala Ser Lys Thr Asn Lys
E--> 12173 65      70      75
12176 <210> SEQ ID NO: 576
12177 <211> LENGTH: 69
12178 <212> TYPE: PRT
12179 <213> ORGANISM: Homo sapiens
12181 <220> FEATURE:
12182 <221> NAME/KEY: unsure
12183 <222> LOCATION: (42)
12184 <223> OTHER INFORMATION: Xaa = Any Amino Acid
12186 <400> SEQUENCE: 576
12187 Met Leu Gly Lys Ser Arg Ala Val Cys Leu Pro Ser Thr Thr Val Thr
12188      5      10      15
12190 Thr Val Cys Tyr Leu Ala Ser Ser Ser Ala Ser Arg Glu Thr Ala Thr
12191      20      25      30
12193 Arg Gln Ala Pro Gly Asn Trp Lys Met Xaa Ser Lys Cys His Ala Gln
12194      35      40      45
12196 Leu Leu Phe Thr Phe Tyr Leu Asn His Phe Tyr Gln Ile Arg Leu Asn
12197      50      55      60
12199 Pro Gly Tyr Ser
E--> 12200 65
12203 <210> SEQ ID NO: 577
12204 <211> LENGTH: 58
12205 <212> TYPE: PRT
12206 <213> ORGANISM: Homo sapiens
12208 <400> SEQUENCE: 577
12209 Met Tyr Leu Glu Asn Ser Phe Tyr Cys Gln Met Ile Leu Leu Lys Arg
12210      5      10      15
12212 Cys Arg Leu Ser Lys Ile Ser Thr Gln Arg Val Val Pro Asp Gly Pro
12213      20      25      30
12215 Pro Ala Pro Val Pro Gly Ser Phe Pro Met Phe Pro Arg Phe Gly Phe
12216      35      40      45
12218 Arg Leu Ala Pro Pro Ala Asp Thr Pro
E--> 12219 50      55
12222 <210> SEQ ID NO: 578
12223 <211> LENGTH: 52
12224 <212> TYPE: PRT
12225 <213> ORGANISM: Homo sapiens
12227 <400> SEQUENCE: 578
12228 Met Gln Leu Ile Tyr Leu Cys Phe Leu Gly Leu Leu Tyr Ile Arg His
12229      5      10      15
12231 His Asp Ser Gln Ser Phe Val Ile Leu Tyr Tyr Lys Lys Leu Asn Tyr
12232      20      25      30
12234 Tyr Phe Lys Tyr Gly Gln Ile Arg Ala Phe His Ile Ala Lys Val Tyr
12235      35      40      45
12237 Gln Pro His

```



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Input Set : A:\42715c15.app  
Output Set : N:\CRF3\06202000\I593793.raw

E--> 12238 50  
12241 <210> SEQ ID NO: 579  
12242 <211> LENGTH: 57  
12243 <212> TYPE: PRT  
12244 <213> ORGANISM: Homo sapiens  
12246 <400> SEQUENCE: 579  
12247 Met His Phe Thr Phe Met Gln Leu Ile Tyr Leu Cys Phe Leu Gly Leu  
12248 5 10 15  
12250 Leu Tyr Ile Arg His His Asp Ser Gln Ser Phe Val Ile Leu Tyr Tyr  
12251 20 25 30  
12253 Lys Lys Leu Asn Tyr Tyr Phe Lys Tyr Gly Gln Ile Arg Ala Phe His  
12254 35 40 45  
12256 Ile Ala Lys Val Tyr Gln Pro His  
E--> 12257 50 55  
15023 <210> SEQ ID NO: 701  
15024 <211> LENGTH: 3228  
15025 <212> TYPE: DNA  
15026 <213> ORGANISM: Homo sapien  
15028 <220> FEATURE:  
15029 <221> NAME/KEY: misc\_feature  
15030 <222> LOCATION: (1)...(3228)  
15031 <223> OTHER INFORMATION: n = A,T,C or G  
15033 <400> SEQUENCE: 701  
E--> 15034  
tccgccccat tgacgcaaat ggcggtaggc gtgtacgggt ggaggtctat ataagcagag 60aactagagaa cccactgctt actggcttat cga:  
E--> 15035 atagggagac ccaagctggc tagcgttttaa acttaagctt ggtaccgagc tcggatccac 180  
E--> 15036 tagtccagtg tgggtgaatt ccattgtgtt gggcaggaaa caagcaaat ggtggagcag 240  
E--> 15037 caagtcaggt gatgtggagc ccagagggtca gggatggctg tctctctagg gtccacttgc 300  
E--> 15038 ccttgtgaga cactttatcc cagcacttta ggaatactga ggtcatacca gccacatctt 360  
E--> 15039 atatgcaaga ttgccagca gagatcaggt ccgagagttc cctttttaaa aaaaggagac 420  
E--> 15040 ttgcttaata aaagaagtct agccacgttt gtgtagagcg gctgtgctgt gctgggggtt 480  
E--> 15041 cacttttgag agagtcttcc tctgagacct gatctctgga ggctgggcaa tcttgcaactt 540  
E--> 15042 gagatggggc tggctgtatc tcagcactcc ttagtctgct cgctctctcc atggccccag 600  
E--> 15043 cctggccaca cctgcttacg gggcactctt agatgccac accataactt ccatgctagt 660  
E--> 15044 ggactgtacc atatcagtg agagctgcag caaggtggcc cctagagcca cgcaccagcc 720  
E--> 15045 tgcacattgc ctctccatac ggcagccctt tatttgaaa cttcctaaat cactttgctg 780  
E--> 15046 tgtgtgttta cacgggtgtg ttttgcctta cttgcccaga gagcacacgg gagtgcagca 840  
E--> 15047 cacaccccaa cccacatcaa ctgccattaa agaaaagaaa ttccagccca gaatttcattg 900  
E--> 15048 tccagcaaaa ttaagcatca taagtgaagg agaaaataaga tccctttcag acaagcaagt 960  
E--> 15049 gctgagggaa tttggtatca ccagatctac cttacgagag ctccctgaagg aagcactaaa 1020  
E--> 15050 tatggaaaga aaagatcatc acctgctact acaaaaacac actgaagtac acagtccaat 1080  
E--> 15051 gatgctaaaa agcaagcaca tatgtaagtc tgcaaaaata ccagctgaca gcatgacgac 1140  
E--> 15052 aggataaaat ccacacatac cttactaac cttaaatgta aatgggctaa atgctcccat 1200  
E--> 15053 tgaagacac ggggcaagct gggtaagaa ccaagaccca ctggagtatg ccgtcttcaa 1260  
E--> 15054 gcaaccatc tcacgtgcag tgccatacat aggtcaaaa taaaggaaatg gagaaaaata 1320  
E--> 15055 tttcaagcaa atggaaaaa gaaaaaagg gttgcactcc cagtttctga caaaacagac 1380  
E--> 15056 tctaccaata aagataaaaa aagagaagga cattacaaag gtggctctga cctttgataa 1440  
E--> 15057 atctcattat tgcttgatac caacctgggc tatttgtatt gcccaaacga ataggataat 1500  
E--> 15058 ttgctgaggt tgtggagctt ctccccttca cagagtcctt gatctccgaa aatttggttg 1560  
E--> 15059 agatgtaagg ttgattttgc tgtacaactc cttttttgaa gttttactca tttccaacaa 1620

*Hand return*

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

*eg. seqs 580, 581, 582, 583-86, 701*

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/593,793  
 DATE: 06/20/2000  
 TIME: 12:41:33

Input Set : A:\42715c15.app  
 Output Set : N:\CRF3\06202000\I593793.raw

```

E--> 15060 ggaaggcaag ttttctgct tccattgaca aaggagagca ggcacctcct ttcctgagtt 1680
E--> 15061 tcagcttgct tctgacaggg aaggagcttt gagatttgaa tactggcctg ctgggttttg 1740
E--> 15062 gacgtgcatt gggcctgttg tcccatttgt gttatttttc tgggaaattt cttccctttg 1800
E--> 15063 gagtgaagaa gcttacccaa tgccctgtacc atcatcgtac cttaaaagaa ctccatttta 1860
E--> 15064 agttcaggga ctccttgga gaagagacgg tagccttgta tcagatcata aaggagaaga 1920
E--> 15065 gcaagaggtc cccggcaaac atccacagat ggccttgga ataagtcacc ttgctcacc 1980
E--> 15066 tgcaggaatg ccagtgaact tattgctgac atcttgagc tcagtacct catagtgtaa 2040
E--> 15067 cggcgtcagc agatctgct gtgctgggac ttcctgtact acccattcct gaggggcat 2100
E--> 15068 gcttctgcag ggcctgtgac ttggtgcaca acttcagaca ccatcatctt gcagcagcac 2160
E--> 15069 cgcacctca ctaccaggg tttgatgac ttctcaagg ccaaggccac attcaaggct 2220
E--> 15070 tcggacttca ttgatgcgt tgtgctgagc aagtggtgct ctccgggac ttaattcagg 2280
E--> 15071 aggtagaatg gagcttgaga tcaagtgtct gatcaagcct cagtgtatgg gcgctgtta 2340
E--> 15072 tcntctggtg ctgaagcagc caagagaccc aagtctgctt ggctgcntct taggatatga 2400
E--> 15073 cagcagagcc agtggcctct actagatcct gtacaacctc aaaaacacc cagacatcgg 2460
E--> 15074 gagtgtgccc agcctgtgat gcaagagtc taatcctgaa gacattgaat gacctgtcat 2520
E--> 15075 tctgctgttt ttacacaaaa ggatcatgag gatcagagag gaaaagtcac ttgcccacaa 2580
E--> 15076 tcacacagct gaacagtgtt ggagtccaac ttgaccctg ggctgtctga cccaagggtg 2640
E--> 15077 tatgcttgct tctctcccaa gagacaactt tcttatcagg ctcaaataaa tgaaaggagg 2700
E--> 15078 atgttaagg taggatctct gaagcctgtt ccagtggaa cgagctcat ggctggcacc 2760
E--> 15079 tgtgtttcca ttctacctc attaagagta aagtttattg agtttattga atttaagtat 2820
E--> 15080 ctttagtgag atcatatatt attagtaaga actgggacca aacagatttt ctgactctaa 2880
E--> 15081 aagagagatt ttacagaaa cagatatata cctgtaagta tacagacacg catacacaca 2940
E--> 15082 tttctttact gctcataaaa attagtcctt attagaatgt gggatgtata aatgtaagag 3000
E--> 15083 aattttcatg ttaaaattga cagatacatt ttaaaattgt ctaaaaaata atttaattat 3060
E--> 15084 tttntttta gaattttcca ttattaatgt tatttttatg agaaactata taactttatt 3120
E--> 15085 gataatacat acaataacce tttgtttttc aaattgaaaa tacagtgtat tttgcaataa 3180
E--> 15086 actaagtcct aattttgtat taaaatttta aattttcaaa aaaaaaaa 3228

```

17350 <210> SEQ ID NO: 778

17351 <211> LENGTH: 1095

17352 <212> TYPE: PRT

17353 <213> ORGANISM: Homo sapiens

17355 <400> SEQUENCE: 778

17356 Met Arg Asn Arg Arg Asn Asp Thr Leu Asp Ser Thr Arg Thr Leu Tyr

17357 5 10 15

17359 Ser Ser Ala Ser Arg Ser Thr Asp Leu Ser Tyr Ser Glu Ser Asp Leu

17360 20 25 30

17362 Val Asn Phe Ile Gln Ala Asn Phe Lys Lys Arg Glu Cys Val Phe Phe

17363 35 40 45

17365 Thr Lys Asp Ser Lys Ala Thr Glu Asn Val Cys Lys Cys Gly Tyr Ala

17366 50 55 60

17368 Gln Ser Gln His Met Glu Gly Thr Gln Ile Asn Gln Ser Glu Lys Trp

17369 65 70 75 80

17371 Asn Tyr Lys Lys His Thr Lys Glu Phe Pro Thr Asp Ala Phe Gly Asp

17372 85 90 95

17374 Ile Gln Phe Glu Thr Leu Gly Lys Lys Gly Lys Tyr Ile Arg Leu Ser

17375 100 105 110

17377 Cys Asp Thr Asp Ala Glu Ile Leu Tyr Glu Leu Leu Thr Gln His Trp

17378 115 120 125

17380 His Leu Lys Thr Pro Asn Leu Val Ile Ser Val Thr Gly Gly Ala Lys

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RAW SEQUENCE LISTING                      DATE: 06/20/2000  
 PATENT APPLICATION: US/09/593,793        TIME: 12:41:34

Input Set : A:\42715c15.app  
 Output Set: N:\CRF3\06202000\I593793.raw

```

17381      130      135      140
17383 Asn Phe Ala Leu Lys Pro Arg Met Arg Lys Ile Phe Ser Arg Leu Ile
17384 145      -      -      150      -      155      -      -      160
17386 Tyr Ile Ala Gln Ser Lys Gly Ala Trp Ile Leu Thr Gly Gly Thr His
17387      165      170      175
17389 Tyr Gly Leu Thr Lys Tyr Ile Gly Glu Val Val Arg Asp Asn Thr Ile
17390      180      185      190
17392 Ser Arg Ser Ser Glu Glu Asn Ile Val Ala Ile Gly Ile Ala Ala Trp
17393      195      200      205
17395 Gly Met Val Ser Asn Arg Asp Thr Leu Ile Arg Asn Cys Asp Ala Glu
17396      210      215      220
17398 Gly Tyr Phe Leu Ala Gln Tyr Leu Met Asp Asp Phe Thr Arg Asp Pro
17399 225      230      235      240
17401 Leu Tyr Ile Leu Asp Asn Asn His Thr His Leu Leu Leu Val Asp Asn
17402      245      250      255
17404 Gly Cys His Gly His Pro Thr Val Glu Ala Lys Leu Arg Asn Gln Leu
17405      260      265      270
17407 Glu Lys His Ile Ser Glu Arg Thr Ile Gln Asp Ser Asn Tyr Gly Gly
17408      275      280      285
17410 Lys Ile Pro Ile Val Cys Phe Ala Gln Gly Gly Gly Lys Glu Thr Leu
17411      290      295      300
17413 Lys Ala Ile Asn Thr Ser Ile Lys Asn Lys Ile Pro Cys Val Val Val
17414 305      310      315      320
17416 Glu Gly Ser Gly Arg Ile Ala Asp Val Ile Ala Ser Leu Val Glu Val
17417      325      330      335
17419 Glu Asp Ala Pro Thr Ser Ser Ala Val Lys Glu Lys Leu Val Arg Phe
17420      340      345      350
17422 Leu Pro Arg Thr Val Ser Arg Leu Ser Glu Glu Glu Thr Glu Ser Trp
17423      355      360      365
17425 Ile Lys Trp Leu Lys Glu Ile Leu Glu Cys Ser His Leu Leu Thr Val
17426      370      375      380
17428 Ile Lys Met Glu Glu Ala Gly Asp Glu Ile Val Ser Asn Ala Ile Ser
17429 385      390      395      400
17431 Tyr Ala Leu Tyr Lys Ala Phe Ser Thr Ser Glu Gln Asp Lys Asp Asn
17432      405      410      415
17434 Trp Asn Gly Gln Leu Lys Leu Leu Leu Glu Trp Asn Gln Leu Asp Leu
17435      420      425      430
17437 Ala Asn Asp Glu Ile Phe Thr Asn Asp Arg Arg Trp Glu Ser Ala Asp
17438      435      440      445
17440 Leu Gln Glu Val Met Phe Thr Ala Leu Ile Lys Asp Arg Pro Lys Phe
17441      450      455      460
17443 Val Arg Leu Phe Leu Glu Asn Gly Leu Asn Leu Arg Lys Phe Leu Thr
17444 465      470      475      480
17446 His Asp Val Leu Thr Glu Leu Phe Ser Asn His Phe Ser Thr Leu Val
17447      485      490      495
17449 Tyr Arg Asn Leu Gln Ile Ala Lys Asn Ser Tyr Asn Asp Ala Leu Leu
17450      500      505      510
17452 Thr Phe Val Trp Lys Leu Val Ala Asn Phe Arg Arg Gly Phe Arg Lys
17453      515      520      525

```

## RAW SEQUENCE LISTING

DATE: 06/20/2000

PATENT APPLICATION: US/09/593,793

TIME: 12:41:34

Input Set : A:\42715c15.app

Output Set: N:\CRF3\06202000\I593793.raw

```

17455 Glu Asp Arg Asn Gly Arg Asp Glu Met Asp Ile Glu Leu His Asp Val
17456      530      535      540
17458 Ser Pro Ile Thr Arg His Pro Leu Gln Ala Leu Phe Ile Trp Ala Ile
17459 545      550      555      560
17461 Leu Gln Asn Lys Lys Glu Leu Ser Lys Val Ile Trp Glu Gln Thr Arg
17462      565      570      575
17464 Gly Cys Thr Leu Ala Ala Leu Gly Ala Ser Lys Leu Leu Lys Thr Leu
17465      580      585      590
17467 Ala Lys Val Lys Asn Asp Ile Asn Ala Ala Gly Glu Ser Glu Glu Leu
17468      595      600      605
17470 Ala Asn Glu Tyr Glu Thr Arg Ala Val Glu Leu Phe Thr Glu Cys Tyr
17471      610      615      620
17473 Ser Ser Asp Glu Asp Leu Ala Glu Gln Leu Leu Val Tyr Ser Cys Glu
17474 625      630      635      640
17476 Ala Trp Gly Gly Ser Asn Cys Leu Glu Leu Ala Val Glu Ala Thr Asp
17477      645      650      655
17479 Gln His Phe Thr Ala Gln Pro Gly Val Gln Asn Phe Leu Ser Lys Gln
17480      660      665      670
17482 Trp Tyr Gly Glu Ile Ser Arg Asp Thr Lys Asn Trp Lys Ile Ile Leu
17483      675      680      685
17485 Cys Leu Phe Ile Ile Pro Leu Val Gly Cys Gly Phe Val Ser Phe Arg
17486      690      695      700
17488 Lys Lys Pro Val Asp Lys His Lys Lys Leu Leu Trp Tyr Tyr Val Ala
17489 705      710      715      720
17491 Phe Phe Thr Ser Pro Phe Val Val Phe Ser Trp Asn Val Val Phe Tyr
17492      725      730      735
17494 Ile Ala Phe Leu Leu Leu Phe Ala Tyr Val Leu Leu Met Asp Phe His
17495      740      745      750
17497 Ser Val Pro His Pro Pro Glu Leu Val Leu Tyr Ser Leu Val Phe Val
17498      755      760      765
17500 Leu Phe Cys Asp Glu Val Arg Gln Trp Tyr Val Asn Gly Val Asn Tyr
17501      770      775      780
17503 Phe Thr Asp Leu Trp Asn Val Met Asp Thr Leu Gly Leu Phe Tyr Phe
17504 785      790      795      800
17506 Ile Ala Gly Ile Val Phe Arg Leu His Ser Ser Asn Lys Ser Ser Leu
17507      805      810      815
17509 Tyr Ser Gly Arg Val Ile Phe Cys Leu Asp Tyr Ile Ile Phe Thr Leu
17510      820      825      830
17512 Arg Leu Ile His Ile Phe Thr Val Ser Arg Asn Leu Gly Pro Lys Ile
17513      835      840      845
17515 Ile Met Leu Gln Arg Met Leu Ile Asp Val Phe Phe Phe Leu Phe Leu
17516      850      855      860
17518 Phe Ala Val Trp Met Val Ala Phe Gly Val Ala Arg Gln Gly Ile Leu
17519 865      870      875      880
17521 Arg Gln Asn Glu Gln Arg Trp Arg Trp Ile Phe Arg Ser Val Ile Tyr
17522      885      890      895
17524 Glu Pro Tyr Leu Ala Met Phe Gly Gln Val Pro Ser Asp Val Asp Gly
17525      900      905      910
17527 Thr Thr Tyr Asp Phe Ala His Cys Thr Phe Thr Gly Asn Glu Ser Lys

```

RAW SEQUENCE LISTING                      DATE: 06/20/2000  
 PATENT APPLICATION: US/09/593,793        TIME: 12:41:34

Input Set : A:\42715c15.app  
 Output Set: N:\CRF3\06202000\I593793.raw

```

17528      915      920      925
17530 Pro Leu Cys Val Glu Leu Asp Glu His Asn Leu Pro Arg Phe Pro Glu
17531      930      935      940
17533 Trp Ile Thr Ile Pro Leu Val Cys Ile Tyr Met Leu Ser Thr Asn Ile
17534 945      950      955      960
17536 Leu Leu Val Asn Leu Leu Val Ala Met Phe Gly Tyr Thr Val Gly Thr
17537      965      970      975
17539 Val Gln Glu Asn Asn Asp Gln Val Trp Lys Phe Gln Arg Tyr Phe Leu
17540      980      985      990
17542 Val Gln Glu Tyr Cys Ser Arg Leu Asn Ile Pro Phe Pro Phe Ile Val
E--> 17543      995      1000      1005
17545 Phe Ala Tyr Phe Tyr Met Val Val Lys Lys Cys Phe Lys Cys Cys Cys
E--> 17546      1010      1015      1020
17548 Lys Glu Lys Asn Met Glu Ser Ser Val Cys Cys Phe Lys Asn Glu Asp
E--> 17549 1025      1030      1035      1040
17551 Asn Glu Thr Leu Ala Trp Glu Gly Val Met Lys Glu Asn Tyr Leu Val
E--> 17552      1045      1050      1055
17554 Lys Ile Asn Thr Lys Ala Asn Asp Thr Ser Glu Glu Met Arg His Arg
E--> 17555      1060      1065      1070
17557 Phe Arg Gln Leu Asp Thr Lys Leu Asn Asp Leu Lys Gly Leu Leu Lys
E--> 17558      1075      1080      1085
17560 Glu Ile Ala Asn Lys Ile Lys
17561      1090      1095
17633 <210> SEQ ID NO: 780
17634 <211> LENGTH: 1095
17635 <212> TYPE: PRT
17636 <213> ORGANISM: Homo sapiens
17638 <220> FEATURE:
17639 <221> NAME/KEY: VARIANT
17640 <222> LOCATION: (1)...(1095)
17641 <223> OTHER INFORMATION: Xaa = Any Amino Acid
17643 <400> SEQUENCE: 780
17644 Met Arg Asn Arg Arg Asn Asp Thr Leu Asp Ser Thr Arg Thr Leu Tyr
17645      5      10      15
17647 Ser Ser Ala Ser Arg Ser Thr Asp Leu Ser Tyr Ser Glu Ser Asp Leu
17648      20      25      30
17650 Val Asn Phe Ile Gln Ala Asn Phe Lys Lys Arg Glu Cys Val Phe Phe
17651      35      40      45
17653 Thr Lys Asp Ser Lys Ala Thr Glu Asn Val Cys Lys Cys Gly Tyr Ala
17654      50      55      60
17656 Gln Ser Gln His Met Glu Gly Thr Gln Ile Asn Gln Ser Glu Lys Trp
17657 65      70      75      80
17659 Asn Tyr Lys Lys His Thr Lys Glu Phe Pro Thr Asp Ala Phe Gly Asp
17660      85      90      95
17662 Ile Gln Phe Glu Thr Leu Gly Lys Lys Gly Lys Tyr Ile Arg Leu Ser
17663      100      105      110
17665 Cys Asp Thr Asp Ala Glu Ile Leu Tyr Glu Leu Leu Thr Gln His Trp
17666      115      120      125
17668 His Leu Lys Thr Pro Asn Leu Val Ile Ser Val Thr Gly Gly Ala Lys

```

*for nos*

*P.30*

## RAW SEQUENCE LISTING

DATE: 06/20/2000

PATENT APPLICATION: US/09/593,793

TIME: 12:41:34

Input Set : A:\42715c15.app

Output Set: N:\CRF3\06202000\I593793.raw

```

17669      130      135      140
17671 Asn Phe Ala Leu Lys Pro Arg Met Arg Lys Ile Phe Ser Arg Leu Ile
17672 145      -150      155      160
17674 Tyr Ile Ala Gln Ser Lys Gly Ala Trp Ile Leu Thr Gly Gly Thr His
17675      165      170      175
17677 Tyr Gly Leu Met Lys Tyr Ile Gly Glu Val Val Arg Asp Asn Thr Ile
17678      180      185      190
17680 Ser Arg Ser Ser Glu Glu Asn Ile Val Ala Ile Gly Ile Ala Ala Trp
17681      195      200      205
17683 Gly Met Val Ser Asn Arg Asp Thr Leu Ile Arg Asn Cys Asp Ala Glu
17684      210      215      220
17686 Gly Tyr Phe Leu Ala Gln Tyr Leu Met Asp Asp Phe Thr Arg Asp Pro
17687 225      230      235      240
17689 Leu Tyr Ile Leu Asp Asn Asn His Thr His Leu Leu Leu Val Asp Asn
17690      245      250      255
17692 Gly Cys His Gly His Pro Thr Val Glu Ala Lys Leu Arg Asn Gln Leu
17693      260      265      270
17695 Glu Lys Tyr Ile Ser Glu Arg Thr Ile Gln Asp Ser Asn Tyr Gly Gly
17696      275      280      285
17698 Lys Ile Pro Ile Val Cys Phe Ala Gln Gly Gly Gly Lys Glu Thr Leu
17699      290      295      300
17701 Lys Ala Ile Asn Thr Ser Ile Lys Asn Lys Ile Pro Cys Val Val Val
17702 305      310      315      320
17704 Glu Gly Ser Gly Gln Ile Ala Asp Val Ile Ala Ser Leu Val Glu Val
17705      325      330      335
17707 Glu Asp Ala Leu Thr Ser Ser Ala Val Lys Glu Lys Leu Val Arg Phe
17708      340      345      350
17710 Leu Pro Arg Thr Val Ser Arg Leu Pro Glu Glu Glu Thr Glu Ser Trp
17711      355      360      365
17713 Ile Lys Trp Leu Lys Glu Ile Leu Glu Cys Ser His Leu Leu Thr Val
17714      370      375      380
17716 Ile Lys Met Glu Glu Ala Gly Asp Glu Ile Val Ser Asn Ala Ile Ser
17717 385      390      395      400
17719 Tyr Ala Leu Tyr Lys Ala Phe Ser Thr Ser Glu Gln Asp Lys Asp Asn
17720      405      410      415
17722 Trp Asn Gly Gln Leu Lys Leu Leu Glu Trp Asn Gln Leu Asp Leu
17723      420      425      430
17725 Ala Asn Asp Glu Ile Phe Thr Asn Asp Arg Arg Trp Glu Ser Ala Asp
17726      435      440      445
17728 Leu Gln Glu Val Met Phe Thr Ala Leu Ile Lys Asp Arg Pro Lys Phe
17729      450      455      460
17731 Val Arg Leu Phe Leu Glu Asn Gly Leu Asn Leu Arg Lys Phe Leu Thr
17732 465      470      475      480
17734 His Asp Val Leu Thr Glu Leu Phe Ser Asn His Phe Ser Thr Leu Val
17735      485      490      495
17737 Tyr Arg Asn Leu Gln Ile Ala Lys Asn Ser Tyr Asn Asp Ala Leu Leu
17738      500      505      510
17740 Thr Phe Val Trp Lys Leu Val Ala Asn Phe Arg Arg Gly Phe Arg Lys
17741      515      520      525

```

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/593,793

DATE: 06/20/2000  
 TIME: 12:41:34

Input Set : A:\42715c15.app  
 Output Set: N:\CRF3\06202000\I593793.raw

17743 Glu Asp Arg Asn Gly Arg Asp Glu Met Asp Ile Glu Leu His Asp Val  
 17744 530 535 540  
 17746 Ser Pro Ile Thr Arg His Pro Leu Gln Ala Leu Phe Ile Trp Ala Ile  
 17747 545 550 555 560  
 17749 Leu Gln Asn Lys Lys Glu Leu Ser Lys Val Ile Trp Glu Gln Thr Arg  
 17750 565 570 575  
 17752 Gly Cys Thr Leu Ala Ala Leu Gly Ala Ser Lys Leu Leu Lys Thr Leu  
 17753 580 585 590  
 17755 Ala Lys Val Lys Asn Asp Ile Asn Ala Ala Gly Glu Ser Glu Glu Leu  
 17756 595 600 605  
 17758 Ala Asn Glu Tyr Glu Thr Arg Ala Val Glu Leu Phe Thr Glu Cys Tyr  
 17759 610 615 620  
 17761 Ser Ser Asp Glu Asp Leu Ala Glu Gln Leu Leu Val Tyr Ser Cys Glu  
 17762 625 630 635 640  
 17764 Ala Trp Gly Gly Ser Asn Cys Leu Glu Leu Ala Val Glu Ala Thr Asp  
 17765 645 650 655  
 17767 Gln His Phe Ile Ala Gln Pro Gly Val Gln Asn Phe Leu Ser Lys Gln  
 17768 660 665 670  
 17770 Trp Tyr Gly Glu Ile Ser Arg Asp Thr Lys Asn Trp Lys Ile Ile Leu  
 17771 675 680 685  
 17773 Cys Leu Phe Ile Ile Pro Leu Val Gly Cys Gly Phe Val Ser Phe Arg  
 17774 690 695 700  
 17776 Lys Lys Pro Val Asp Lys His Lys Lys Leu Leu Trp Tyr Tyr Val Ala  
 17777 705 710 715 720  
 17779 Phe Phe Thr Ser Pro Phe Val Val Phe Ser Trp Asn Val Val Phe Tyr  
 17780 725 730 735  
 17782 Ile Ala Phe Leu Leu Phe Ala Tyr Val Leu Leu Met Asp Phe His  
 17783 740 745 750  
 17785 Ser Val Pro His Pro Pro Glu Leu Val Leu Tyr Ser Leu Val Phe Val  
 17786 755 760 765  
 17788 Leu Phe Cys Asp Glu Val Arg Gln Trp Tyr Val Asn Gly Val Asn Tyr  
 17789 770 775 780  
 17791 Phe Thr Asp Leu Trp Asn Val Met Asp Thr Leu Gly Leu Phe Tyr Phe  
 17792 785 790 795 800  
 17794 Ile Ala Gly Ile Val Phe Arg Leu His Ser Ser Asn Lys Ser Ser Leu  
 17795 805 810 815  
 17797 Tyr Ser Gly Arg Val Ile Phe Cys Leu Asp Tyr Ile Ile Phe Thr Leu  
 17798 820 825 830  
 17800 Arg Leu Ile His Ile Phe Thr Val Ser Arg Asn Leu Gly Pro Lys Ile  
 17801 835 840 845  
 17803 Ile Met Leu Gln Arg Met Leu Ile Asp Val Phe Phe Phe Leu Phe Leu  
 17804 850 855 860  
 17806 Phe Ala Xaa Trp Met Val Ala Phe Gly Val Ala Arg Gln Gly Ile Leu  
 17807 865 870 875 880  
 17809 Arg Gln Asn Glu Gln Arg Trp Arg Trp Ile Phe Arg Ser Val Ile Tyr  
 17810 885 890 895  
 17812 Glu Pro Tyr Leu Ala Met Phe Gly Gln Val Pro Ser Asp Val Asp Gly  
 17813 900 905 910  
 17815 Thr Thr Tyr Asp Phe Ala His Cys Thr Phe Thr Gly Asn Glu Ser Lys

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/593,793

DATE: 06/20/2000  
 TIME: 12:41:34

Input Set : A:\42715c15.app  
 Output Set: N:\CRF3\06202000\I593793.raw

```

17816          915          920          925
17818 Pro Leu Cys Val Glu Leu Asp Glu His Asn Leu Pro Arg Phe Pro Glu
17819      .930.          .935          .940
17821 Trp Ile Thr Ile Pro Leu Val Cys Ile Tyr Met Leu Ser Thr Asn Ile
17822 945          950          955          960
17824 Leu Leu Val Asn Leu Leu Val Ala Met Phe Gly Tyr Thr Val Gly Thr
17825          965          970          975
17827 Val Gln Glu Asn Asn Asp Gln Val Trp Lys Phe Gln Arg Tyr Phe Leu
17828          980          985          990
17830 Val Gln Glu Tyr Cys Ser Arg Leu Asn Ile Pro Phe Pro Phe Ile Val
E--> 17831          995          1000          1005
17833 Phe Ala Tyr Phe Tyr Met Val Val Lys Lys Cys Phe Lys Cys Cys Cys
E--> 17834      1010          1015          1020
17836 Lys Glu Lys Asn Met Glu Ser Ser Val Cys Cys Phe Lys Asn Glu Asp
E--> 17837 1025          1030          1035          1040
17839 Asn Glu Thr Leu Ala Trp Glu Gly Val Met Lys Glu Asn Tyr Leu Val
E--> 17840          1045          1050          1055
17842 Lys Ile Asn Thr Lys Ala Asn Asp Thr Ser Glu Glu Met Arg His Arg
E--> 17843          1060          1065          1070
17845 Phe Arg Gln Leu Asp Thr Lys Leu Asn Asp Leu Lys Gly Leu Leu Lys
E--> 17846          1075          1080          1085
17848 Glu Ile Ala Asn Lys Ile Lys
17849          1090          1095

```

*fix nos.*

*1st*

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.



VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/593,793

DATE: 06/20/2000  
TIME: 12:41:35

Input Set : A:\42715c15.app  
Output Set : N:\CRF3\06202000\I593793.raw

L:26 M:270 C: Current Application Number differs, Wrong Format  
L:27 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:53 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:54 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:55 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:57 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:79 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:80 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:81 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:82 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:83 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2  
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3  
L:126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:131 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:133 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4  
L:158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:185 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:203 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:208 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:211 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:230 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:232 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:234 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:235 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:236 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

VERIFICATION SUMMARY                      DATE: 06/20/2000  
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Input Set : A:\42715c15.app  
Output Set: N:\CRF3\06202000\I593793.raw

L:237 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:238 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:252 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:699 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3  
L:1470 M:283 W: Missing Blank Line separator, <400> field identifier  
L:7338 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:378  
M:332 Repeated in SeqNo=378  
L:7714 M:252 E: No. of Seq. differs, <211>LENGTH:Input:155 Found:154 SEQ:383  
L:9546 M:252 E: No. of Seq. differs, <211>LENGTH:Input:141 Found:140 SEQ:477  
L:9580 M:252 E: No. of Seq. differs, <211>LENGTH:Input:144 Found:143 SEQ:478  
L:9629 M:252 E: No. of Seq. differs, <211>LENGTH:Input:223 Found:222 SEQ:479  
L:9663 M:252 E: No. of Seq. differs, <211>LENGTH:Input:145 Found:144 SEQ:480  
L:9706 M:252 E: No. of Seq. differs, <211>LENGTH:Input:168 Found:167 SEQ:481  
L:9740 M:252 E: No. of Seq. differs, <211>LENGTH:Input:144 Found:143 SEQ:482  
L:9774 M:252 E: No. of Seq. differs, <211>LENGTH:Input:144 Found:143 SEQ:483  
L:10021 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:502  
L:10021 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:502  
L:10021 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:502  
L:10021 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:502  
L:10021 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:502  
L:10022 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:502  
L:10022 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:502  
L:10022 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:502  
L:10022 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:502  
M:340 Repeated in SeqNo=502  
L:10023 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:502  
L:10023 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:502  
L:10023 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:502  
L:10023 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:502  
L:10024 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:502  
L:10024 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:502  
L:10024 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:502  
L:10024 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:502  
L:10026 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:502  
L:10026 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:502  
L:10026 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:502  
L:10026 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:502  
L:10034 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503  
L:10034 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503  
L:10034 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503  
L:10034 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503  
L:10034 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:503  
L:10035 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503  
L:10035 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503  
L:10035 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503  
L:10035 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503  
M:340 Repeated in SeqNo=503  
L:10036 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503

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L:10036 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503  
L:10036 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503  
L:10036 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503  
L:10038 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503  
L:10038 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503  
L:10038 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503  
L:10038 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503  
L:10039 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503  
L:10039 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503  
L:10039 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503  
L:10039 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503  
L:10040 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:503  
L:10040 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:503  
L:10040 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:503  
L:10040 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:503  
L:10110 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:508  
L:10110 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:508  
L:10110 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:508  
L:10110 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:508  
L:10110 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:508  
L:10324 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:523  
L:10324 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:523  
L:10324 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:523  
L:10331 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:523  
L:10390 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:525  
L:10480 M:252 E: No. of Seq. differs, <211>LENGTH:Input:321 Found:320 SEQ:527  
L:10619 M:252 E: No. of Seq. differs, <211>LENGTH:Input:293 Found:292 SEQ:532  
L:10698 M:252 E: No. of Seq. differs, <211>LENGTH:Input:267 Found:266 SEQ:534  
L:11118 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:537  
M:332 Repeated in SeqNo=537  
L:11160 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1229 Found:1228 SEQ:537  
L:11355 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:538  
M:332 Repeated in SeqNo=538  
L:11403 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1262 Found:1261 SEQ:538  
L:11562 M:252 E: No. of Seq. differs, <211>LENGTH:Input:15 Found:11 SEQ:551  
L:12151 M:252 E: No. of Seq. differs, <211>LENGTH:Input:63 Found:62 SEQ:574  
L:12173 M:252 E: No. of Seq. differs, <211>LENGTH:Input:77 Found:76 SEQ:575  
L:12200 M:252 E: No. of Seq. differs, <211>LENGTH:Input:69 Found:68 SEQ:576  
L:12219 M:252 E: No. of Seq. differs, <211>LENGTH:Input:58 Found:57 SEQ:577  
L:12238 M:252 E: No. of Seq. differs, <211>LENGTH:Input:52 Found:51 SEQ:578  
L:12257 M:252 E: No. of Seq. differs, <211>LENGTH:Input:57 Found:56 SEQ:579  
L:12279 M:252 E: No. of Seq. differs, <211>LENGTH:Input:68 Found:67 SEQ:580  
L:12301 M:252 E: No. of Seq. differs, <211>LENGTH:Input:78 Found:77 SEQ:581  
L:12320 M:252 E: No. of Seq. differs, <211>LENGTH:Input:52 Found:51 SEQ:582  
L:12339 M:252 E: No. of Seq. differs, <211>LENGTH:Input:61 Found:60 SEQ:583  
L:12361 M:252 E: No. of Seq. differs, <211>LENGTH:Input:77 Found:76 SEQ:584  
L:12380 M:252 E: No. of Seq. differs, <211>LENGTH:Input:51 Found:50 SEQ:585  
L:12399 M:252 E: No. of Seq. differs, <211>LENGTH:Input:61 Found:60 SEQ:586  
L:15034 M:254 E: No. of Bases conflict, LENGTH:Input:120 Counted:110 SEQ:701

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L:15034 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2

M:254 Repeated in SeqNo=701

- L:15086 M:252 E: No. of Seq. differs, &lt;211&gt;LENGTH:Input:3228 Found:3218 SEQ:701

L:17543 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:778

M:332 Repeated in SeqNo=778

L:17831 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:780

M:332 Repeated in SeqNo=780